WHAT IS CLAIMED IS:

1. A method of identifying genes essential to growth of a selected organism comprising:

(a) preparing a genomic library of a selected organism;

(b) providing a plurality of identical grids, each grid comprising a surface on which is immobilized at predefined regions on said surface a plurality of defined materials derived from the genomic library;

(c) mutagenizing the selected organism;

(d) growing a test culture comprising mutagenized selected organism and a control culture comprising non-mutagenized selected organism under a set of defined conditions;

(e) harvesting surviving cells from the cultures;

(f) extracting and isolating DNA from harvested cells of the test culture;

(g) extracting and isolating RNA or DNA from harvested cells of the control culture;

(h) generating labeled polynucleotide probes from the isolated DNA of the test culture;

(i) generating labeled polynucleotide probes from the isolated RNA or DNA of the control culture;

(j) hybridizing the labeled probes generated from the isolated DNA of the test culture to a first identical grid to produce a test hybridization pattern;

(k) hybridizing the labeled probes generated from the isolated RNA or DNA of the control culture to a second identical grid to produce a control hybridization pattern;

(l) comparing the hybridization patterns to identify genes essential for growth of the selected organism; and

(m) confirming that said identified gene is essential for growth of the selected organism.

2. The method of claim 1 wherein essential genes are identified in step (l) by determining differences between the test hybridization pattern and the control hybridization pattern.

3. The method of claim 1 wherein the set of defined conditions of step (d) comprises standard non-pathogenic *in vitro* culture conditions for the selected organism.

4. The method of claim 1 wherein the set of defined conditions of step (d) comprises *in vitro* conditions which reflect or mimic *in vivo*, pathogenic settings such as aerobic or anaerobic conditions, auxotrophic, heat-shock, osmotic-shock, addition or presence of antibiotics or drugs, carbon source variations, and *in vivo* pathogenic conditions.

5. The method of claim 1 wherein the harvesting of surviving cells of step (e) is performed during early logarithmic growth.

6. The method of claim 1 wherein the harvesting of surviving cells of step (e) is performed during late logarithmic growth.

7. The method of claim 1 wherein the harvesting of surviving cells of step (e) is performed during stationary phase growth.

8. The method of claim 1 wherein the harvesting of surviving cells of step (e) is performed during late stationary phase growth.

9. The method of claim 1 wherein:

step (d) further comprises growing additional test and control cultures under a different set of defined conditions; and

step (l) comprises comparing test and control hybridization patterns from the cells grown under the different sets of defined conditions.

10. The method of claim 9 wherein genes essential to the selected organism are identified by determining identical hybridization patterns for all of the cells grown under the different sets of defined conditions.

11. The method of claim 9 wherein genes essential to the selected organism are identified by determining differences between the test and control hybridization patterns for cells grown under the different sets of defined conditions.

12. A method of identifying genes essential to growth of a selected organism by identifying conditionally lethal mutant genes, which comprises:

(a) preparing a genomic library of a selected organism: (*i*) in an integration vector; or (*ii*) in an expression vector;

(b) providing a grid comprising a surface on which is immobilized at predefined regions on said surface a plurality of defined materials derived from the genomic library;

(c) mutagenizing the selected organism;

(d) growing the mutagenized organism under permissive and non-permissive conditions to identify mutagenized organisms containing conditionally lethal mutant genes;

(e) transforming such organisms containing said conditionally lethal mutant genes with the genomic library of step (a);

(f) growing the transformed cells under the same non-permissive conditions as step (d) to identify transformed cells in which conditionally lethal mutant genes have been complemented;

(g) harvesting surviving cells;

(h) extracting and isolating DNA from the harvested cells;

(i) generating labeled polynucleotide probes from the isolated DNA;

(j) hybridizing the labeled probes generated from the isolated DNA to a grid, whereby such probes that hybridize to the grid identify genes essential for growth of the selected organism.

13. An isolated gene sequence which is essential to growth of a selected organism which is identified by the method of claim 1.

14. An isolated protein produced by expression of a gene sequence of claim 13.

15. A therapeutic compound capable of modulating expression of the gene sequence of claim 13 for use in the treatment of a disease associated with growth of an organism.

16. A therapeutic compound capable of modulating activity of a protein of claim 14 for use in the treatment of a disease associated with growth of an organism.

17. A diagnostic composition useful for the diagnosis of a disease or infection comprising a reagent capable of detectably targeting a gene sequence of claim 13.

18. An isolated gene sequence which is essential to growth of a selected organism which is identified by the method of claim 12.

19. An isolated protein produced by expression of a gene sequence of claim 18.

20. A therapeutic compound capable of modulating expression of the gene sequence of claim 18 for use in the treatment of a disease associated with growth of an organism.

21. A therapeutic compound capable of modulating activity of a protein of claim 19 for use in the treatment of a disease associated with growth of an organism.

22. A diagnostic composition useful for the diagnosis of a disease or infection comprising a reagent capable of detectably targeting a gene sequence of claim 18.